OIPE

RAW SEQUENCE LISTING   DATE: 07/02/2002
PATENT APPLICATION: US/10/054,712   TIME: 13:53:04

Input Set : N:\Crf3\RULE60\10054712.raw
Output Set: N:\CRF3\07022002\J054712.raw

SEQUENCE LISTING

```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Gerald R. Crabtree
 6                     Schreiber, Stuart L.
 7                     Spencer, David M.
 8                     Wandless, Thomas J.
 9                     Belshaw, Peter
11     (ii) TITLE OF INVENTION: Regulated Apoptosis
13    (iii) NUMBER OF SEQUENCES: 81
15     (iv) CORRESPONDENCE ADDRESS:
16          (A) ADDRESSEE: ARIAD Pharmaceuticals, Inc.
17          (B) STREET: 26 Landsdowne Street
18          (C) CITY: Cambridge
19          (D) STATE: Massachusetts
20          (E) COUNTRY: USA
21          (F) ZIP: 02139
23      (v) COMPUTER READABLE FORM:
24          (A) MEDIUM TYPE: Floppy disk
25          (B) COMPUTER: IBM PC compatible
26          (C) OPERATING SYSTEM: PC/DOS/MS/DOS
27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29     (vi) CURRENT APPLICATION DATA:
30          (A) APPLICATION NUMBER: US/10/054,712
31          (B) FILING DATE: 13-Nov-2001
32          (C) CLASSIFICATION:
34    (vii) PRIOR APPLICATION DATA:
36          (A) APPLICATION NUMBER: US/09/302,629
37          (B) FILING DATE:
39          (A) APPLICATION NUMBER: 09/087,811
40          (B) FILING DATE:
42   (viii) ATTORNEY/AGENT INFORMATION:
43          (A) NAME: Figg, E. Anthony
44          (B) REGISTRATION NUMBER: 27,195
45          (C) REFERENCE/DOCKET NUMBER: 2054-108A
47     (ix) TELECOMMUNICATION INFORMATION:
48          (A) TELEPHONE: (202) 783-6040
49          (B) TELEFAX: (202) 783-6031
52 (2) INFORMATION FOR SEQ ID NO: 1:
54      (i) SEQUENCE CHARACTERISTICS:
55          (A) LENGTH: 14 amino acids
56          (B) TYPE: amino acid
57          (D) TOPOLOGY: linear
59     (ii) MOLECULE TYPE: peptide
```

C--> 30
C--> 31

ENTERED

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```
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
65       Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
66         1             5                 10
69 (2) INFORMATION FOR SEQ ID NO: 2:
71      (i) SEQUENCE CHARACTERISTICS:
72              (A) LENGTH: 11 base pairs
73              (B) TYPE: nucleic acid
74              (C) STRANDEDNESS: single
75              (D) TOPOLOGY: linear
77     (ii) MOLECULE TYPE: cDNA
81     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
83       GTTAAGTTAA C                                          11
85 (2) INFORMATION FOR SEQ ID NO: 3:
87      (i) SEQUENCE CHARACTERISTICS:
88              (A) LENGTH: 11 base pairs
89              (B) TYPE: nucleic acid
90              (C) STRANDEDNESS: single
91              (D) TOPOLOGY: linear
93     (ii) MOLECULE TYPE: cDNA
97     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
99       TGACTCAGCG C                                          11
101 (2) INFORMATION FOR SEQ ID NO: 4:
103       (i) SEQUENCE CHARACTERISTICS:
104              (A) LENGTH: 33 base pairs
105              (B) TYPE: nucleic acid
106              (C) STRANDEDNESS: single
107              (D) TOPOLOGY: linear
109     (ii) MOLECULE TYPE: cDNA
112     (ix) FEATURE:
113              (A) NAME/KEY: misc_feature
114              (B) LOCATION: 6..11
115              (D) OTHER INFORMATION: /note= "Sac II restriction site."
117     (ix) FEATURE:
118              (A) NAME/KEY: misc_signal
119              (B) LOCATION: 12..16
120              (D) OTHER INFORMATION: /note= "Kozak sequence."
122     (ix) FEATURE:
123              (A) NAME/KEY: CDS
124              (B) LOCATION: 17..31
126     (ix) FEATURE:
127              (A) NAME/KEY: misc_feature
128              (B) LOCATION: 17..33
129              (D) OTHER INFORMATION: /note= "Region of homology with
130 target sequence."
134     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
136       CGACACCGCG GCCACC ATG GCC ACA ATT GGA GC                33
137                         Met Ala Thr Ile Gly
138                          1             5
141 (2) INFORMATION FOR SEQ ID NO: 5:
```

RAW SEQUENCE LISTING
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```
143        (i) SEQUENCE CHARACTERISTICS:
144              (A) LENGTH: 5 amino acids
145              (B) TYPE: amino acid
146              (D) TOPOLOGY: linear
148        (ii) MOLECULE TYPE: protein
150        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
152         Met Ala Thr Ile Gly
153          1                5
155 (2) INFORMATION FOR SEQ ID NO: 6:
157        (i) SEQUENCE CHARACTERISTICS:
158              (A) LENGTH: 27 base pairs
159              (B) TYPE: nucleic acid
160              (C) STRANDEDNESS: single
161              (D) TOPOLOGY: linear
163        (ii) MOLECULE TYPE: cDNA
166        (ix) FEATURE:
167              (A) NAME/KEY: misc_feature
168              (B) LOCATION: 6..11
169              (D) OTHER INFORMATION: /note= "Xho I restriction site."
171        (ix) FEATURE:
172              (A) NAME/KEY: misc_feature
173              (B) LOCATION: 12..27
174              (D) OTHER INFORMATION: /note= "Region of homology with
175 target sequence."
178        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
180         CGACACTCGA GAGCCCATGA CTTCTGG                    27
182 (2) INFORMATION FOR SEQ ID NO: 7:
184        (i) SEQUENCE CHARACTERISTICS:
185              (A) LENGTH: 4 amino acids
186              (B) TYPE: amino acid
187              (C) STRANDEDNESS: single
188              (D) TOPOLOGY: linear
190        (ii) MOLECULE TYPE: peptide
193        (ix) FEATURE:
194              (A) NAME/KEY: Peptide
195              (B) LOCATION: 1..4
196              (D) OTHER INFORMATION: /note= "Translation product of
197 complement of SEQ ID NO:6, bases 9 to 20."
201        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
203         Ser Trp Ala Leu
204          1
206 (2) INFORMATION FOR SEQ ID NO: 8:
208        (i) SEQUENCE CHARACTERISTICS:
209              (A) LENGTH: 41 base pairs
210              (B) TYPE: nucleic acid
211              (C) STRANDEDNESS: single
212              (D) TOPOLOGY: linear
214        (ii) MOLECULE TYPE: cDNA
217        (ix) FEATURE:
```

```
218              (A) NAME/KEY: misc_feature
219              (B) LOCATION: 6..11
220              (D) OTHER INFORMATION: /note= "Xho I restriction site."
222      (ix) FEATURE:
223              (A) NAME/KEY: misc_feature
224              (B) LOCATION: 12..41
225              (D) OTHER INFORMATION: /note= "Region of homology with
226 target sequence."
228      (ix) FEATURE:
229              (A) NAME/KEY: CDS
230              (B) LOCATION: 9..41
232      (ix) FEATURE:
233              (A) NAME/KEY: misc_feature
234              (B) LOCATION: 28
235              (D) OTHER INFORMATION: /note= "A to G."
238      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
240      CGACACTC GAG CTC TGC TAC TTG CTA GGT GGA ATC CTC TTC            41
241              Glu Leu Cys Tyr Leu Leu Gly Gly Ile Leu Phe
242               1           5                    10
245 (2) INFORMATION FOR SEQ ID NO: 9:
247      (i) SEQUENCE CHARACTERISTICS:
248              (A) LENGTH: 11 amino acids
249              (B) TYPE: amino acid
250              (D) TOPOLOGY: linear
252      (ii) MOLECULE TYPE: protein
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
256        Glu Leu Cys Tyr Leu Leu Gly Gly Ile Leu Phe
257          1           5                    10
259 (2) INFORMATION FOR SEQ ID NO: 10:
261      (i) SEQUENCE CHARACTERISTICS:
262              (A) LENGTH: 24 base pairs
263              (B) TYPE: nucleic acid
264              (C) STRANDEDNESS: single
W--> 288          (D) TOPOLOGY: /note= "Translational stop encoded
289                            in complementary strand."
267      (ii) MOLECULE TYPE: cDNA
269      (ix) FEATURE:
270              (A) NAME/KEY: misc_feature
271              (B) LOCATION: 3..8
272              (D) OTHER INFORMATION: /note= "Eco RI restriction site."
274      (ix) FEATURE:
275              (A) NAME/KEY: misc_feature
276              (B) LOCATION: 9..24
277              (D) OTHER INFORMATION: /note= "Region of homology with
278 target sequence."
280      (ix) FEATURE:
281              (A) NAME/KEY: misc_feature
282              (B) LOCATION: 24
283              (D) OTHER INFORMATION: /note= "G to C."
```

```
285      (ix) FEATURE:
286            (A) NAME/KEY: misc_signal
287            (B) LOCATION: complement (9..11)
292      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
294      GCGAATTCTT AGCGAGGGGC CAGC                                    24
296 (2) INFORMATION FOR SEQ ID NO: 11:
298       (i) SEQUENCE CHARACTERISTICS:
299            (A) LENGTH: 4 amino acids
300            (B) TYPE: amino acid
301            (C) STRANDEDNESS: single
302            (D) TOPOLOGY: linear
304      (ii) MOLECULE TYPE: peptide
307      (ix) FEATURE:
308            (A) NAME/KEY: Peptide
309            (B) LOCATION: 1..4
310            (D) OTHER INFORMATION: /note= "Translational product of
311 complement to SEQ ID NO:10, bases 12 to 23."
314      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
316      Leu Ala Pro Arg
317      1
319 (2) INFORMATION FOR SEQ ID NO: 12:
321       (i) SEQUENCE CHARACTERISTICS:
322            (A) LENGTH: 33 base pairs
323            (B) TYPE: nucleic acid
324            (C) STRANDEDNESS: single
W--> 343       (D) TOPOLOGY: /note= "Translational stop signal
344                         encoded on complementary strand."
327      (ii) MOLECULE TYPE: cDNA
330      (ix) FEATURE:
331            (A) NAME/KEY: misc_feature
332            (B) LOCATION: 3..8
333            (D) OTHER INFORMATION: /note= "Eco RI restriction."
335      (ix) FEATURE:
336            (A) NAME/KEY: misc_feature
337            (B) LOCATION: 12..17
338            (D) OTHER INFORMATION: /note= "Sal I restriction site."
340      (ix) FEATURE:
341            (A) NAME/KEY: misc_signal
342            (B) LOCATION: complement (9..11)
353      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
355      GCGAATTCTT AGTCGACGCG AGGGGCCAGG GTC                          33
357 (2) INFORMATION FOR SEQ ID NO: 13:
359       (i) SEQUENCE CHARACTERISTICS:
360            (A) LENGTH: 4 amino acids
361            (B) TYPE: amino acid
362            (C) STRANDEDNESS: single
363            (D) TOPOLOGY: linear
365      (ii) MOLECULE TYPE: peptide
368      (ix) FEATURE:
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/02/2002
PATENT APPLICATION: US/10/054,712   TIME: 13:53:05

Input Set : N:\Crf3\RULE60\10054712.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:69; N Pos. 12,13,14,15,16,17,18,19,20
Seq#:70; Xaa Pos.3,4,5
Seq#:71; N Pos.. 41,42,43,44,45,46,47,48,49
Seq#:72; Xaa Pos.13,14,15
Seq#:73; N Pos. 37,38,39,40,41,42,43,44,45
Seq#:74; Xaa Pos.9,10,11

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/054,712

DATE: 07/02/2002
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Input Set : N:\Crf3\RULE60\10054712.raw
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:288 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:288 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=10
L:343 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:343 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=12
L:1691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
L:1755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0